

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: February 3, 2003, 12:50:42 ; Search time 2379 Seconds

(without alignments)  
17563.832 Million cell updates/sec

Title: US-10-047-593-5  
Perfect score: 2580  
Sequence: 1 gcggcgccgctaacagacc.....cgctctaggaaggctacgct 2580

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

EST:  
1: em\_ebca:\*  
2: em\_esthm:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	511	19.8	547	17	BH619556
C 2	427.4	16.6	717	17	BH838358
C 3	338	13.1	677	17	BH800632
C 4	335.4	13.0	727	17	BH838131
C 5	323.6	12.5	485	17	BH779556
C 6	319.4	12.4	509	17	BH127535

Result No.	Score	Query Match	Length DB	ID	Description
C 7	309.8	12.0	744	17	BH837342
C 8	308.6	12.0	617	17	BH774273
C 9	305.2	11.8	847	17	BH129403
C 10	297	11.5	710	17	BH837822
C 11	289.2	11.2	709	17	BH837873
C 12	288.4	11.2	549	17	BH774554
C 13	284.2	11.0	620	17	BH836722
C 14	283.2	11.0	813	17	BH839302
C 15	282.2	10.9	618	17	BH837660
C 16	281.6	10.9	606	17	BH837437
C 17	278	10.8	378	17	BH772161
C 18	277.2	10.7	546	17	BH785550
C 19	277.2	10.7	719	17	BH838303
C 20	273.2	10.6	522	17	BH130068
C 21	269.8	10.5	533	17	A2920086
C 22	268.4	10.4	729	17	BH839096
C 23	266.6	10.3	535	17	BH222651
C 24	266.2	10.3	926	17	BH128342
C 25	263.2	10.2	844	17	BH129231
C 26	262.2	10.2	697	17	BH837902
C 27	260.4	10.1	995	17	BH129116
C 28	252.6	9.8	592	17	BH786386
C 29	251.6	9.8	455	17	BH837520
C 30	247.8	9.6	605	17	BH782172
C 31	246.6	9.6	445	17	A2921056
C 32	245.6	9.5	280	17	BH619555
C 33	243.4	9.4	593	17	BH773010
C 34	243.4	9.4	831	17	BH12782
C 35	242.6	9.4	455	17	BH807089
C 36	240.8	9.3	867	17	BH127930
C 37	240	9.3	742	17	BH140491
C 38	239	9.3	473	17	BH779949
C 39	236.4	9.2	365	17	BH128264
C 40	233	9.0	729	17	BH876361
C 41	232.2	9.0	925	17	BH128803
C 42	229.2	8.9	681	17	BH255865
C 43	228.8	8.9	557	17	BH773008
C 44	225.8	8.8	443	17	BH129668
C 45	224.4	8.7	735	17	BH836993

## ALIGNMENTS

RESULT 1  
LOCUS BH619556/c 547 bp DNA linear GSS 30-JAN-2002  
DEFINITION 1007059F11.y1 1007 - Rescuedu Grid H Zea mays genomic, DNA  
SEQUENCE  
ACCESSION BH619556  
VERSION BH619556.1 GI:18430399  
KEYWORDS  
SOURCE GSS.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
Clade; Panicoideae; Andropogonaceae; Zea.  
1 (bases 1 to 547)  
Walbot, V.  
Maize genomic sequences found using engineered Rescuedu transposon  
Unpublished (2001)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Possible ligation site so sequence was trimmed. Post-ligation  
sequence submitted separately.  
Plate: 1007059 column: 19  
Class: transposon-tagged  
Location/Qualifiers

## FEATURES

source

1. .547  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/B73"  
 /db\_xref="taxon:4577"  
 /clone\_1lb="1007" - RescuedMu Grid H"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf; Vector: RescuedMu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; RescuedMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transposon web units. For more information on RescuedMu, go to the site 'www.zmhd.iastate.edu' and follow the links for 'RescuedMu.' Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT 179 a 114 c 97 g 157 t  
 ORIGIN

Query Match 19.8%; Score 511; DB 17; Length 547;  
 Best Local Similarity 97.1%; Pred. No. 2.1e-113;  
 Matches 531; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 1521 CAATTGTCATTTATTTTTCCTTCCATTAAC-AAACGAAAGTACCTGTTTTT 1579  
 DB 547 CAATTGTCATTTATTTTTCCTTCCATTAACAAAGTACCTGTTTTT 488  
 QY 1580 TGGACCTTTGACACATACCTTTTAAAGTATTCACAAATTAAGCTTTATGTAAC 1639  
 DB 487 TGGACCTTTGACACATACCTTTTAAAGTATTCACAAATTAAGCTTTATGTAAC 428  
 QY 1640 AAACATTTTGGAGAGGCTGATTGAGAGAAAGTGCCTGATGATTCATTAAGAC 1699  
 DB 427 AAGCTAATTTGAGAGAGGCTGATTGAGAGAAAGTGCCTGATGATTCATTAAGAC 368  
 QY 1700 GAAATCGATGTTAAATGCTGTTGATTAATTTCTAGCTTACACGCTGTTGAACG 1759  
 DB 367 GAAATCGATGTTAAATGCTGTTGATTAATTTCTAGCTTACACGCTGTTGAACG 308  
 QY 1760 CGTAGAAGTGTGGAATTCCTCTATGATTAATTAAGTGAAGTTTGTACAGTT 1819  
 DB 307 CGTAGAAGTGTGGAATTCCTCTATGATTAATTAAGTGAAGTTTGTTCAGTT 248  
 QY 1820 TATTTACGATTCATTAACGATTTTATTAGGATTCGTTGACATTAATTCAGCTTTT 1879  
 DB 247 TATTTACGATTCATTAACGATTTTATTAGGATTCGTTGACATTAATTCAGCTTTT 188  
 QY 1880 TTTTAAATGTCACAAAGAACTTTTCAACACCTAAGTGAAGTAAAGAAACATGAC 1939  
 DB 187 TTTTAAATGTCACAAAGAACTTTTCAACACCTAAGTGAAGTAAAGAAACATGAC 128  
 QY 1940 AATTTGATTTTGAAGAAATATGACAGATTAAGTGTGTGGGACCGTAGAGATAG 1999  
 DB 127 AATTTGATTTTGAAGAAATATGACAGATTAAGTGTGTGGGACCGTAGAGATAG 68  
 QY 2000 AGAGATGAGAGACGAGCGGACGACGACCTTCCGATTTGCCGTGACATCCTTGG 2059  
 DB 67 AGAGATGAGAGACGAGCGGACGACGACCTTCCGATTTGCCGTGACATCCTTGG 8  
 QY 2060 TCAGGGG 2066  
 DB 7 TCAGGGG 1

RESULT 2  
 BH838358 717 bp DNA linear GSS 28-MAY-2002  
 LOCUS BH838358  
 DEFINITION LMCRI00011F01f Zea mays L. Zea mays genomic clone LMCRI00011F01f,  
 DNA sequence.

ACCESSION BH838358  
 VERSION BH838358.1 GI:21236236  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 717)  
 Kim, S.W., Yu, Y., Lee, M.C., Main, D. and Wing, R.A.  
 Methy1-Filteration genomic sequence from maize  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: twing@clemson.edu  
 Total High Quality bases = 428  
 Seg primer: TAATACACTCACTATAGG  
 Class: shotgun  
 High quality sequence start: 44  
 High quality sequence stop: 686.  
 Location/Qualifiers  
 1. .717  
 /organism="Zea mays"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="LMCRI00011F01f"  
 /clone\_1lb="Zea mays L."  
 /tissue\_type="leaf"  
 /lab\_host="DH10B"  
 /note="Vector: pGEM-T easy; Site 1: Mcr BC; Methy1-Filteration library; Nuclei DNA was completely digested with Mcr BC, size fractionated and transformed to E.Coli.DH10B."

BASE COUNT 147 a 223 c 169 g 175 t 3 others  
 ORIGIN

Query Match 16.6%; Score 427.4; DB 17; Length 717;  
 Best Local Similarity 90.5%; Pred. No. 4.4e-93;  
 Matches 497; Conservative 0; Mismatches 31; Indels 21; Gaps 3;

QY 37 TTGGATCTCTTCCTTATTTTGGGAAAGCCGACCGTTGGGACCGTTGGCGCA 96  
 DB 149 TGGGATCTCTTCCTTATTTTGGGAAAGCCGACCGTTGGGACCGTTGGCGCA 208  
 QY 97 CCGGACACTGTCGGGTGACACCGGACAGTCAGTGCCTTCGACCGTTGGCTCGC 156  
 DB 209 CCGGACACTGTCGGGTGACACCGGACAGTCAGTGCCTTCGACCGTTGGCTCGC 268  
 QY 157 CACGCTTTCGCGGAGATCGGCGGACAGCGTTGGCGCGACCGACCGTTGGCTCA 216  
 DB 269 CACGCTTTCGCGGAGATCGGCGGACAGCGTTGGCGCGACCGACCGTTGGCTCA 327  
 QY 217 ACAGTCCGTGACACAGACAGTCGCGGTATTAATAGCCGTACCGCTTAATCACTTC 276  
 DB 328 -----GACAGTCGCGGTATTAATAGCCGTACCGCTTAATCACTTC 369  
 QY 277 CGAGAGACGAAGTTGCGCTGAGACGACCTGCGGACCGGACACGTCGTCCGTAACACC 336  
 DB 370 CGAGAGACGAAGTTGCGCTGAGACGACCTGCGGACCGGACACGTCGTCCGTAACACC 429  
 QY 337 GGACAGTCGCGGTGACCCGAGTCAGAGCTGACTTGGCTGAACAAAGTCATCTTAATGTC 396  
 DB 430 GTACAGTCGCGGTGACCCGAGTCAGAGCTGACTTGGCTGAACAAAGTCATCTTAATGTC 489  
 QY 397 AACTGATTTTTCCTGTTTCCAGACCTTAAGCAATTAATAGCTCTTAACAAATGTA 456  
 DB 490 AACTGATTTTTCCTGTTTCCAGACCTTAAGCAATTAATAGCTCTTAAACAAATGTA 548  
 QY 457 TTAATTTGAGAAACATACCTTAATTAATCTGTTGTGTAATCTTGTCCACCAATTAACACTTG 516

Db 549 CTAACTCTGAGAAACATCTTTACTTGATTTGTCTGACCATTTTACACTTA 608  
 Qy 517 GGCAC-TTGTGTGGACACTAAATCAACCAATCTTGAATAGCCCAAGGACATTT 575  
 Db 609 GGCACTTGTGTGGACACTAAATCAACCAATCTTGAATAGCCCAAGGACATTT 668  
 Qy 576 CCGCTTCA 584  
 Db 669 TCCCTTCA 677

RESULT 3  
 BH800632/c 677 bp DNA linear GSS 25-APR-2002  
 LOCUS 1008125G09.x1 1008 - RescuenMu Grid I Zea mays genomic, DNA  
 DEFINITION  
 sequence.  
 ACCESSION BH800632  
 VERSION BH800632.1 GI:20312874  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 677)  
 Walbot, V.  
 Maize genomic sequences found using engineered RescuenMu transposon  
 Unpublished (2001)  
 CONTACT: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 723 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 plate: 1008125 row: 15  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1..677  
 /organism="Zea mays"  
 /cultivar="mixed background W23/A188/873"  
 /db\_xref="taxon:4577"  
 /clone\_lib="1008 - RescuenMu Grid I"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /note="Organ: leaf, Vector: RescuenMu (engineered from  
 pBluescript backbone); Site\_1: BamHI, Site\_2: BglII;  
 RescuenMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescuenMu, go to the web  
 site www.zmhd.iastate.edu and follow the links for  
 'RescuenMu.' Grid I was grown at Berkeley in 2001. DNA was  
 extracted from leaf punches, double digested using BamHI  
 and BglII, and ligated to form circular plasmids. DH10B  
 cells were transformed and then screened on LB plates with  
 ampicillin."

BASE COUNT 201 a 134 c 160 g 182 t  
 ORIGIN  
 Query Match 13.1%; Score 338; DB 17; Length 677;  
 Best Local Similarity 97.0%; Pred. No. 2,4e-71;  
 Matches 355; Conservative 0; Mismatches 10; Indels 1; Gaps 1;  
 Qy 1922 TAAAGAAAAAAGCATGATTTGAAAAAAGAAATGACAGATTAAGCTTT 1981  
 Db 366 TAAAGAAAAAAGCATGATTTGAAAAAAGAAATGACAGATTAAGCTTT 307  
 Qy 1982 GGGAGCCGTAGAGACTTAGAGAGATGAGACGCGCAGAGAGAGCTTGGATTG 2041

Db 306 GGGAGATGGGAGCCGTAGAGAGATGAGACGCGCAGAGAGAGCTTGGATTG 247  
 Qy 2042 CCGTCAGCTCAACCTGTGTGAGGCGCTCACTTGAAGAGATTAAGAGGAGCTTCA 2101  
 Db 246 CCGTCAGCTCAACCTGTGTGAGGCGCTCACTTGAAGAGATTAAGAGGAGCTTCA 187  
 Qy 2102 GTTTCTCTCAATAGCGCGGAAATATCTGAGATTTCTTGA-TTTTTTACTTGTAT 2160  
 Db 186 GTTTCTCTCAATAGCGCGGAAATATCTGAGATTTCTTGA-TTTTTTACTTGTAT 127  
 Qy 2161 TCTATTCCTCTCCGCGCGCTCTAGTCTATTCTCTCTCCGTCGAGTGTGCTTC 2220  
 Db 126 TCTATTCCTCTCCGCGCGCTCTAGTCTATTCTCTCTCCGTCGAGTGTGCTTC 67  
 Qy 2221 TTGATCCACTTTTCCCGCATCTCTATCTCCCTTCAAGGAGCTGTTCCTCC 2280  
 Db 66 TTGATCCACTTTTCCCGCATCTCTATCTCCCTTCAAGGAGCTGTTCCTCC 7  
 Qy 2281 GGACTC 2286  
 Db 6 GGACTC 1

RESULT 4  
 BH838131 727 bp DNA linear GSS 28-MAY-2002  
 LOCUS LMCRI00008H10f Zea mays L. Zea mays genomic clone LMCRI00008H10f,  
 DEFINITION  
 DNA sequence.  
 ACCESSION BH838131  
 VERSION BH838131.1 GI:21236009  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 727)  
 Klm, S.W., Yu, Y., Lee, M.C., Main, D. and Wing, R.A.  
 MethyI-filtration genomic sequence from maize  
 Unpublished (2002)  
 CONTACT: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: twing@clemson.edu  
 Total High Quality bases = 561  
 Seq primer: TAATACGACTCACTATAGG  
 Class: shotgun  
 High quality sequence start: 30  
 High quality sequence stop: 714.  
 Location/Qualifiers  
 1..727  
 /organism="Zea mays"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="LMCRI00008H10f"  
 /clone\_lib="Zea mays L."  
 /tissue\_type="leaf"  
 /lab\_host="DH10B"  
 /note="Vector: pGEM-T easy; Site 1: Mcr BC;  
 MethyI-filtration library; Nuclei DNA was completely  
 digested with Mcr BC, size fractionated and transformed  
 to E.Coli.DH10B."

FEATURES  
 source  
 BASE COUNT 161 a 211 c 173 g 177 t 5 others  
 ORIGIN  
 Query Match 13.0%; Score 335.4; DB 17; Length 727;  
 Best Local Similarity 81.5%; Pred. No. 1e-70;  
 Matches 446; Conservative 0; Mismatches 76; Indels 25; Gaps 4;

QY 39 CGAGTCTCTTCTTATTGCGAGCCGACCGTGGC-GCTTGAAGCCGTTGGCGCAC 97  
 125 CTGATTTCTTCTTAAATGCGAGCCGACCGTGGCAGACTTGGACCGTGGCGCAC 184  
 QY 98 CGGACATCTCCGCTGACACCGGACAGTGGCCCTCCGACCGTGGCTGGCC 157  
 185 CGGACA-TGTCGGGTGACACCGGACAGTGGCTGGACATCTTTCAGCCGTTGCTAGCC 243  
 QY 158 ACGTGTTCGCGCGATCGCGCGACCGTGGCCGACCGACCGTGGCTTCA 217  
 244 ATGATCTTGGCGAGATTGGCGCGCCGCTGGCCCGGCGACCGTGGCTTCA 303  
 QY 218 CAGTCCGCTGACACCGACAGTCCGCTGAATTATACCGCTGACCGTGGCTTCA 277  
 304 CAGTCCGCTGACACCGACAGTCCGCTGAATTATACCGCTGACCGTGGCTTCA 363  
 QY 278 GAGAGCAGCAGTTCGCTGACCGCGACCGTGGCGACCGTGGCTGACACCG 337  
 364 GAGAGCAGCAGTTCGCTGACCGCGACCGTGGCGACCGTGGCTGACACCG 423  
 QY 338 GACAGTCCGCTGACACCGACAGTGGCTTGGCTGACCGTGGCTTCA 397  
 424 CTGACGAGATTCTGGCTGCTGACCGCAA-----GACATTTTCCA 462  
 QY 398 ACTGATTTTCTGTTTCCGACCTTACACCAATACCTTATCTTAAACAAATGAT 457  
 463 ATTGAATTTTCTGTTTCCGACCTTACACCAATACCTTATCTTAAACAAATGAT 522  
 QY 458 TAATCTGAGAAACATACCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 517  
 523 TTAGCTGAGAAACATACCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 582  
 QY 518 GCATCTGTTGGACATTAATCAACAAATCTTAAAGTGGCGCGACCGTGGCTTCC 577  
 583 ACATCTGTTGG--ACTTAATCAACAAACATTAAGTGGCGCGACCGTGGCTTCC 640  
 Db 578 CTTTCAA 584  
 QY 641 CTTTCAA 647

RESULT 5  
 BH779556/c 485 bp DNA linear GSS 28-MAR-2002  
 LOCUS f2mb014f016a12f0 f2mb filtered library Zea mays genomic clone  
 DEFINITION f2mb014f016a12 5', DNA sequence.

ACCESSION BH779556  
 VERSION BH779556  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.

REFERENCE  
 AUTHORS Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N. and Lakey, N.D.  
 TITLE Genethresher methylation filtered genomic sequences from maize  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Bedell JA  
 Orion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: f2mb014f016 row: e column: 12  
 Seq primer: M13 forward  
 Class: shotgun

FEATURES  
 source High quality sequence stop: 485.

Location/Qualifiers  
 1..485  
 /organism="Zea mays"  
 /cultivar="MO17"  
 /db\_xref="taxon:4577"

/clone="f2mb014f016a12"  
 /clone\_id="f2mb filtered library"  
 /note="Organ: leaf; Vector: pBSC(-); Site 1: HincII; DNA  
 prepared from purified nuclei was randomly sheared,  
 end-repaired, size fractionated to enrich for the 0.5 to  
 5 kb fraction, ligated into HincII-digested pBSC(-)  
 vector and electroporated into E. coli cells."  
 BASE COUNT 125 a 97 c 145 g 117 t 1 others  
 ORIGIN

Query Match 12.5%; Score 323.6; DB 17; Length 485;  
 Best Local Similarity 84.5%; Pred. No. 7.5e-66;  
 Matches 393; Conservative 0; Mismatches 55; Indels 17; Gaps 2;

QY 126 TCAGTGGCCCTTCCGACCGTGGCTGGCGACGTTGTCGCGGATCCGCGGACGA 185  
 485 TCGGTCGCTTCCGACCGTGGCTGGCGACGTTGTCGCGGATCCGCGGACGA 430  
 Db 186 CCGTGGCCCGGACCGACCGTGGCTGGCGACGTTGTCGCGGATCCGCGGAT 245  
 429 -----CCGACCGTGGCTTCCGACCGTGGCTGGCGACGTTGTCGCGGAT 382  
 QY 246 GAATTAATAGCCGTAGCGCGTTATACCTTCCGAGAGAGAGTGGCTGAGCGACGC 305  
 381 GAATTAATAGCGGTAGCGCGTTATACCTTCCGAGAGAGAGTGGCTGAGCGACGC 322  
 QY 306 TGGCGACCGGACCACTGTCCGCTGACCAACCGACAGTCCGCTGACCGACGCTG 365  
 321 TGGCGACCGGACCACTGTCCGCTGACCAACCGACAGTCCGCTGACCGACGCTG 262  
 QY 366 ACTTGGCTGAAACAAATGATCTTATGTTCACTTATTTTCTGTTTCCAGACTTA 425  
 261 GCTTGGCTGAAACAAAGG-TATCTCTCCAAATTTGTTTCTGTTTCCAGACTTA 203  
 QY 426 GACAAATACATTAATGCTTAAACAAATGATTAATGCTGAGAAACATACCTTATCT 485  
 202 GACAAATACATTAATGCTTAAACAAATGATTAATGCTGAGAAACATACCTTATCT 143  
 Db 486 GATTGATCTTGTCCACCACTTAAACATCTTGGGCACTTGTGGACACTTAATCA 545  
 142 GATTGATCTTGTCCACCACTTAAACATCTTGGGCACTTGTGGACACTTAATCA 83  
 QY 546 AATACCTTAAATGCGCGACCGTGGCTGGCGACGTTGTCGCGGATCCGCGGAC 590  
 82 AACACTTAAATGCGCGACCGTGGCTGGCGACGTTGTCGCGGATCCGCGGAC 38  
 Db

RESULT 6  
 BH127535 509 bp DNA linear GSS 23-JUL-2001  
 LOCUS G-1h2.r Maize Random Small-Insert Genomic Library Zea mays genomic  
 DEFINITION clone G-1h2 both, DNA sequence.

ACCESSION BH127535  
 VERSION BH127535  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.

REFERENCE  
 AUTHORS Meyers, B.C., Tingey, S.V. and Morgante, M.  
 TITLE Abundance, distribution and transcriptional activity of repetitive  
 elements in the maize genome  
 JOURNAL Genome Res. 11 (10), 1660-1676 (2001)  
 MEDLINE 21475670  
 COMMENT Contact: Morgante M  
 Suite 200  
 Dupont Genomics  
 PO Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302 631 2638  
 Fax: 302 631 2607  
 Email: Michele.morgante@usa.dupont.com

Sequences were trimmed to include only high quality bases; forward and reverse reads were assembled when significant overlaps were detected.

Seq primer: M13reverse  
Class: shotgun.

FEATURES  
Location/Qualifiers  
1..509

BASE COUNT 101 a 156 c 126 g 126 t

Query Match 12.4%; Score 319.4; DB 17; Length 509;  
Best Local Similarity 84.8%; Pred. No. 7.8e-67;  
Matches 401; Conservative 0; Mismatches 51; Indels 21; Gaps 3;

37 TTGGATCTCTCTCTATTGCGGAAGCCGCTGGCGC-CTTGGAGCCGTTGGCGC 95  
57 TGGGATTTCTCTCTATTGCGGAAGCCGCTGGCGC-CTTGGAGCCGTTGGCGC 116  
96 ACCGACACTGTCGGGTGACACCGGACAGTGGGCCCCCTTCCGACCGTGGGCTCGG 155  
117 ACCGACACTGTCGGGTGACACCGGACAGTGGGCCCCCTTCCGACCGTGGGCTCGG 176  
156 CCAAGTGTTCGGCGCGAGTGGCGGACGCGTGGCGCGACCGGCGTGGGCTCGG 215  
177 CCAAGTGTTCGGCGCGAGTGGCGGACGCGTGGCGCGACCGGCGTGGGCTCGG 236  
216 GACAGTCCGGTGCACACGAGTCCGGTGAATTATAGCCGTTAATCACTTC 275  
237 -----GACAGTCCGGTGAATTATAGCCGTTAATCACTTC 277  
276 CCGAGACAGCAAGTTCGCTGAGCAGCCTGGCGGACCGGACAGTTCGGGTAACAC 335  
278 CCGAGACAGCAAGTTCGCTGAGCAGCCTGGCGGACCGGACAGTTCGGGTAACAC 337  
336 CCGAGACAGTCCGGTGCACACGAGTGAAGTGGTGAACAAAGTCACTTATTC 395  
338 CCGAGACAGTCCGGTGCACACGAGTGAAGTGGTGAACAAAGTCACTTATTC 396  
396 CCACTGATTTTCTCTCTATTGCGGAAGCCGCTGGCGC-CTTGGAGCCGTTGGCGC 455  
397 CAACTGATTTTCTCTCTATTGCGGAAGCCGCTGGCGC-CTTGGAGCCGTTGGCGC 456  
456 AATTAATCTGAGAAACATACCTTATATCTGTTGTAATTGTCCACCATTT 508  
457 ACTAAGTCTGAGAAACATACCTTATATCTGTTGTAATTGTCCACCATTT 509

RESULT 7  
BH837342 744 bp DNA linear GSS 28-MAY-2002  
LOCUS LMCRO50012G12F Zea mays L. Zea mays genomic clone LMCRO50012G12F,  
DEFINITION DNA sequence.  
ACCESSION BH837342  
VERSION BH837342.1 GI:21235220  
KEYWORDS GSS.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 744)

AUTHORS Kim,S.W., Yu,Y., Lee,M.C., Main,D. and Wing,R.A.  
TITLE Methyl-filteration genomic sequence from maize  
JOURNAL Unpublished (2002)  
COMMENT Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu

FEATURES  
source  
Total High Quality bases = 573  
Seq primer: TAAATGACATCTACATAGGCG  
Class: shotgun  
High quality sequence start: 7  
High quality sequence stop: 725.  
Location/Qualifiers  
1..744  
/organism="Zea mays"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="LMCRO50012G12F"  
/clone\_lib="Zea mays L."  
/tissue\_type="leaf"  
/lab\_host="DH10B"  
/note="Vector: pGEM-T easy; Site 1: Msc BC;  
Methyl-filteration library. Nuclei DNA was completely  
digested with Msc BC, size fractionated and transformed  
to E.Coli.DH10B."

BASE COUNT 147 a 217 c 215 g 160 t 5 others

Query Match 12.0%; Score 309.8; DB 17; Length 744;  
Best Local Similarity 86.5%; Pred. No. 1.7e-64;  
Matches 366; Conservative 0; Mismatches 52; Indels 5; Gaps 2;

37 TTGGATCTCTCTCTATTGCGGAAGCCGCTGGCGC-CTTGGAGCCGTTGGCGC 96  
140 TGGGATTTCTCTCTATTGCGGAAGCCGCTGGCGC-CTTGGAGCCGTTGGCGC 199  
97 CCGAGACAGTTCGCTGAGCAGCCTGGCGGACCGGACAGTTCGGGTAACAC 156  
200 CCGAGACAGTTCGCTGAGCAGCCTGGCGGACCGGACAGTTCGGGTAACAC 259  
157 CAGGTGTTCGGCGGATGCGCGGACAGCCTGGCGGACCGGACAGTTCGGGTAACAC 216  
260 CAGGTGTTCGGCGGATGCGCGGACAGCCTGGCGGACCGGACAGTTCGGGTAACAC 315  
217 ACAATCCGGTGCACACGAGTCCGGTGAATTATAGCCGTTAATCACTTC 276  
316 ACAATCCGGTGCACACGAGTCCGGTGAATTATAGCCGTTAATCACTTC 375  
277 CGAGAGCAGCAAGTTCGCTGAGCAGCCTGGCGGACCGGACAGTTCGGGTAACAC 336  
376 CGAGAGCAGCAAGTTCGCTGAGCAGCCTGGCGGACCGGACAGTTCGGGTAACAC 435  
436 GGAACAGTCCGGTGCACACGAGTGAAGTGGTGAACAAAGTCACTTATTC 494  
437 GGAACAGTCCGGTGCACACGAGTGAAGTGGTGAACAAAGTCACTTATTC 494  
397 AACTGATTTTCTCTCTATTGCGGAAGCCGCTGGCGC-CTTGGAGCCGTTGGCGC 456  
495 AATTAATCTGAGAAACATACCTTATATCTGTTGTAATTGTCCACCATTT 554  
457 TTA 459  
555 CTA 557

RESULT 8  
BH774273 617 bp DNA linear GSS 28-MAR-2002  
LOCUS uzmb003f006b02K0 uzmb unfiltered library Zea mays genomic clone  
DEFINITION uzmb003f006b02 5', DNA sequence.

Accession	Version	Source	Organism	Reference	Authors	Title	Journal	Comment
BH774273	BH774273.1	GI:19776302	Zea mays.					
KEYWORDS	GSS:		Zea mays.					
ORGANISM			Zea mays.					
REFERENCE			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.					
AUTHORS			1 (bases 1 to 617)					
TITLE			Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N., and Lakey, N.D.					
JOURNAL			Genethresher methylation filtered genomic sequences from maize Unpublished (2002)					
COMMENT			Contact: Bedell, JA Orion Genomics, LLC 4041 Forest Park Ave, St. Louis, MO 63108, USA Tel: 314 615 6979 Fax: 314 615 5975 Email: jbedell@oriongenomics.com Plate: uzmb003f006 row: b column: 02 Seq primer: SK reverse Class: shotgun					
FEATURES			High quality sequence scrop: 617.					
source			Location/Qualifiers					
			1..617					
			/organism="Zea mays"					
			/cultivar="MO17"					
			/db xref="taxon:4577"					
			/clone="uzmb003f006b02"					
			/clone_1lb="uzmb unfiltered library"					
			/note="Organ: leaf; Vector: pBCKS(-); Site_1: HincII; DNA prepared from purified nuclei was randomly sheared, 0.5 to 5 kb fraction, ligated into HincII-digested pBCKS(-) vector and electroporated into E. coli cells."					
BASE COUNT	155 a	155 c	181 g	126 t				
ORIGIN								
Query Match	12.0%;	Score 308.6;	DB 17;	Length 617;				
Best Local Similarity	77.5%;	Pred. No. 3.3e-64;						
Matches 441;	Conservative 0;	Mismatches 114;	Indels 14;	Gaps 5				
39	CGGATCTTCCTTCTTATTTGGCGAAGCCGACCGCTTGGCGCT-TTGGAGCCGTTGGCGAC	97						
607	CCGATGTGTTTCCCTTAATGGCGAAGCCGACCGCTTGGACATCTGAGAGCCGTGACGAC	548						
98	CGGACATGTCGCGGTGACACCGGACAGTCAGGTGACCCCTTCCGACCGTGTGCTCGGCC	157						
547	CGGACA-TGTTCCGTGACACCGGACAGTCCGGTGCCCCCTTCCGACCGTGTGCTGCCC	489						
158	ACGTGTTTCGCGCGGATGCGCGGCGACGCGTGGCCCGGACCGACCGTGGCTACCGGA	217						
488	ACGTGTGCGCGCGAAGATCCGCGGCGACCGTGGCTGCGCGACCGTGGCTCACCGGA	429						
218	CAGTCCGCTGACACACGACAGTCCGGTGAATTATAGCGGTATACCGCTTATACCTTCC	277						
428	CAGTCCGCTGACACCGGACAGTCCGGTGAATTATAGCGGTATACCGCTTATACCTTCC	369						
278	GAGAGCAGCAAGTTCGCTGAGCCGCTGAGCCGCGACCGGACACTGTCCGCTGAACCACG	337						
368	GAGAGCGGCTTTCGCGCGAGGACGCTGCGGACCGGACACTGTCCGCTGACCAACG	309						
338	GACAGTCCGCTGACCCGAGTCAAGTCTGAGTGAACCAAGTCACTTTAGTTCCA	397						
308	GACAGTCCGCTGACCCGAGTCAAGTCTGAGTGAACCAAGTCACTTTAGTTCCA	249						
398	ACTTGATTTTCTGTTTTCGACACTTGAACCAATATAGTCTTAAACATGTAT	457						
248	TTCTTTTCTTCTTCGTTTCCATATCTTGAACAAGTATATAGTACACCAAACTATGAC	189						
458	TAATCTGAGAA-CATGACCTTATAGTCTGTTTACTTTGTCACC-----AT	506						
188	TAAAGCTTGAAGAACATATCTTGTCTTGAATTGTCACCTTGTCCATCATGATGGATAGA	129						

OY	507	TTTCACTGGGACCTGTGTGGAGACTAAATCACCAATAATTAGAATGCCCAAG	566
Db	128	TTTCATTTAAGACCGTGTTGG-CACTGAATCACAATAATCTTAGAATGCCCAAG	70
OY	567	GGCACATTTCCCTTCAACAGTCGGTGC	595
Db	69	GGCACATTTCCCTTCAATCTCGCATGC	41
RESULT 9			
BH129403		847 bp	DNA linear GSS 23-JUL-2001
DEFINITION		G-5c8 Maize Random Small-insert Genomic library Zea mays genomic clone G-5c8 both, DNA sequence.	
ACCESSION		BH129403	
VERSION		BH129403.1	
KEYWORDS		GI:14997719	
SOURCE		GSS.	
ORGANISM		Zea mays.	
COMMENT		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 847) Meyer, B.C., Tingey, S.V. and Morgante, M. Abundance, distribution and transcriptional activity of repetitive elements in the maize genome Genome Res. 11 (10), 1660-1676 (2001) 21475670 Contact: Morgante M Suite 200 Dupont Genomics PO Box 6104, Newark, DE 19714-6104, USA Tel: 302 631 2638 Fax: 302 631 2607 Email: michel.morgante@usa.dupont.com Sequences were trimmed to include only high quality bases; forward and reverse reads were assembled when significant overlaps were detected. Seq primer: MJ3univ and MJ3reverse Class: shotgun.	
FEATURES			
source		location/Qualifiers	
		1..847	
		/organism="Zea mays"	
		/strain="B73"	
		/db_xref="taxon:4577"	
		/clone="G-5c8"	
		/library="Maize Random Small-insert Genomic Library"	
		/sex="hermaphrodite"	
		/tissue_type="leaf"	
		/cell_type="Young Leaf"	
		/dev_stage="seedling"	
		/note="Vector: pCR-Script; Total genomic DNA was nebulized / ends were polished with Pfu polymerase and the fragments cloned into PCR-Script."	
BASE COUNT		163 a 252 c 230 g 189 t 13 others	
ORIGIN			
Query Match		11.8%; Score 305.2; DB 17; Length 847;	
Best Local Similarity		77.1%; Pred. No. 2.3e-63;	
Matches 431; Conservative		0; Mismatches 114; Indels 14; Gaps 5	
OY	39	CGGATCTCTTCTTCTTATTGTTGGGAGACCGACCGTTGGCGCT-TTGGAGCGCTTGGCGCAC	97
Db	25	CGGATCTCTTCTTCTTAAATGCGCACCGACCGTTGCAATCTGGAGCGCTTGGCGCAC	84
OY	98	CGGACACTGTCGGTGCAACCGGACAGTCAAGTGGCCCCCTTCCGACGCTTGGCTCGGCC	157
Db	85	CGGACA-TGTGCGGTGCACACCGGACAGTCCGGTG-CCCCTTCCGACGCTTGGCTCGGCC	142
OY	158	ACGTGTTGGCGCGGATCGGCGGCGACAGCCGTTGGCGCGACCGACCGGTTGGGCTCAACGGA	217
Db	143	ACGTGTCGCGCACGAGATTTCGCGGCGGACCGCTTGGCGCGGACCGGCTTGGCTCAACGGA	202



Qy 218 CAGTCCGCTGCAACACCAAGTCCGTTGAATATAGCCGTACCGCTTAATCACTTCCC 277  
 Db 203 CAGTCCGCTGCAACACCAAGTCCGTTGAATATAGCCGTACCGCTTGAATTTCCC 262  
 Qy 278 GAGACGACCAAGTGGCGTGGCCGCTGGCGGACCCGGAACACTGTCCGTTGAACACCG 337  
 Db 253 GAGACGCGGCTGCTTGGCCGAGTGGCTGGCGGACCCGGAACACTGTCCGTTGAACACCG 322  
 Qy 338 GACAGTCCGCTGCAACACCAAGTCCGTTGAATATAGCCGTACCGCTTAATCACTTCCC 397  
 Db 323 GACAGTCCGCTGCAACACCAAGTCCGTTGAATATAGCCGTACCGCTTGAATTTCCC 382  
 Qy 398 ACTGATTTTCTGTTTCCGACCACTTAAGACAAATATAGTCTCTTAACCAATATAT 457  
 Db 383 TTTNNNTTCTTCTGTTTNNATCTNNNACAGTATATAGTACACAAACCAATATAT 442  
 Qy 458 TAATTCGAGAAACATACCTTATATAGTCTTGAATTTGATCTTCTC-----CACAT 507  
 Db 443 TAAGCTTGAAGAACTATCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGT 502  
 Qy 508 TTAACCTTGGGCTGTTGTTGACACTTAATCAACAAATATAGTAAATGGCCCAAG 567  
 Db 503 TCACATTTAAGCACTTGTGTTGG-CACATCAATCAACAAATATAGTAAATGGCCCAAG 561  
 Qy 568 GCACATTTCCCTTCAACA 586  
 Db 562 GCACATTTCCCTTCAACA 580

RESULT 10  
 BH837822 710 bp DNA linear GSS 28-MAY-2002  
 LOCUS LMCRI00004D12f Zea mays L. Zea mays genomic clone LMCRI00004D12f,  
 DEFINITION DNA sequence.  
 ACCESSION BH837822 GI:21235700  
 VERSION BH837822.1  
 KEYWORDS GSS.

## SOURCE

ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 1 (bases 1 to 710)

REFERENCE Kim, S.W., Yu, Y., Lee, M.C., Main, D. and Wing, R.A.  
 TITLE Methyl-filtration genomic sequence from maize  
 JOURNAL Unpublished (2002)

COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: twing@clemson.edu

FEATURES  
 source  
 1. 710  
 Location/Qualifiers  
 High quality sequence start: 7  
 High quality sequence stop: 686.

BASE COUNT 136 a 224 c 166 g 184 t  
 ORIGIN  
 /organism="Zea mays"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="LMCRI00004D12f"  
 /clone\_1lb="Zea mays L."  
 /tissue\_type="Leaf"  
 /lab\_host="DH10B"  
 /note="Vector: pGEM-T easy; Site 1: Mcr BC;  
 Methyl-filtration library; Nuclei DNA was completely  
 digested with Mcr BC. Size fractionated and transformed  
 to E.Coli DH10B."

Query Match 11.5%; Score 297; DB 17; Length 710;  
 Best Local Similarity 75.4%; Pred. No. 2.2e-61;  
 Matches 426; Conservative 0; Mismatches 125; Indels 14; Gaps 4;

Qy 39 CGATATCTCTTCTTATTTGGGGAAGCCGATGCGTGGG-CGCTTGGAGCGTTGGCGCAC 97  
 Db 123 CGATATCTCTTCTTATTTGGGGAAGCCGATGCGTGGG-CGCTTGGAGCGTTGGCGCAC 182  
 Qy 98 CGGACACTGTCCGCTGACACCGGACAGTCAAGTCAAGTCCCGCTTCCGACCGTGGCTGGCC 157  
 Db 183 CGGACA-TGTTGGGTGACACCGGACAGTCCGCTCCCGCTTCTTGAAGCGTGGCTGGCC 241  
 Qy 158 ACGTGT--TTCCGGGAGATCCGCGGCGGACAGTCCGCTTCCGACCGTGGCTGGCC 215  
 Db 242 ACGTGTCTCTTTTATTTTATTCGCGCGGCGGACAGTCCGCTTCCGACCGTGGCTGGCC 301  
 Qy 216 GACAGTCCGCTGACACCGGACAGTCAAGTCAAGTCCCGCTTCCGACCGTGGCTGGCC 275  
 Db 302 GACAGTCCGCTGACACCGGACAGTCCGCTTCCGACCGTGGCTGGCC 361  
 Qy 276 CGGAGACGACGAAATTCGCTGAGCCGCTGGCGGACCGGACGACTGTCCGTTGAACAC 335  
 Db 362 CGGAGGCGGCGCACTTCCGCTGAGGCGGACCGGACCGGACGACTGTCCGTTGAACAC 421  
 Qy 336 CGGACAGTCCGCTGACACCGGACAGTCAAGTCAAGTCCCGCTTCCGACCGTGGCTGGCC 395  
 Db 422 CGGACAGTCCGCTGACACCGGACAGTCAAGTCAAGTCCCGCTTCCGACCGTGGCTGGCC 481  
 Qy 396 CAATCTGATTTTCTCTGTTTCCGACCACTTAAGACAAATATAGTCTTAAACCAATGT 455  
 Db 482 TTTTCTTCTCTTCTTCTGTTTCTTAAATATAGTAAATATAGTAAACCAATGT 541  
 Qy 456 ATTAATTTCTGAGAAACATACCTTTATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 505  
 Db 542 ACTAAGACTTTAAGACATACCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 601  
 Qy 506 TTTAACCTTGGGCGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 565  
 Db 602 ATTCACTTTAAGCACTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 661  
 Qy 566 GGGCACATTTCCCTTCAACAGTCC 590  
 Db 662 GGGCACATTTCCCTTCAACATCTCC 686

RESULT 11  
 BH837873 709 bp DNA linear GSS 28-MAY-2002  
 LOCUS LMCRI00005D09f Zea mays L. Zea mays genomic clone LMCRI00005D09f,  
 DEFINITION DNA sequence.  
 ACCESSION BH837873  
 VERSION BH837873.1 GI:21235751  
 KEYWORDS GSS.

SOURCE Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 1 (bases 1 to 709)

REFERENCE Kim, S.W., Yu, Y., Lee, M.C., Main, D. and Wing, R.A.  
 TITLE Methyl-filtration genomic sequence from maize  
 JOURNAL Unpublished (2002)

COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: twing@clemson.edu  
 Total High Quality bases = 452  
 Seq primer: TTAATGACTCACTATAGG  
 Class: shotgun

High quality sequence start: 60  
High quality sequence stop: 555.  
Location/Qualifiers

## FEATURES

source

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/organism="Zea mays"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="LMCR10005D09E"  
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/lab host="DH10B"  
/note="Vector: pGEM-T easy; Site 1: Msc BC;  
Methyl-fragmentation library; Nuclei DNA was completely  
digested with Msc BC, size fractionated and transformed  
to E.Coli DH10B."

BASE COUNT 165 a 188 c 203 g 152 t 1 others  
ORIGIN

Query Match 11.2%; Score 289.2; DB 17; Length 709;  
Best Local Similarity 74.5%; Pred. No. 1.8e-59;  
Matches 408; Conservative 0; Mismatches 128; Indels 12; Gaps 3;

39 CGATCTCTCTCTTATTGCGAAGCCGACCGTTGGCGCTTTGAGCCGTTGGCGACC 98  
647 CGGATCTCTCTTAAAGATGTAAGGCTGACCAATGAGGATGGAGACGTTGGCGCA-C 589  
99 GGAACCTCTCGGTGACACCGGACGTCAGTCCGCTTCCGACCGTTGGCGCGCA 158  
588 GGTGAGGGGGGGTGCACACGAAACAGCGCGTCCCGCTTCGACCGTTGGCGCA 529  
159 CGTGTTCGCGCGGATCGCGCGGACCGTTGGCGCGACCGTTGGCGCTACCGGAC 218  
528 CGTGTTCGCGCGGATCGCGCGGACCGTTGGCGCGACCGTTGGCGCTACCGGAC 469  
219 AGTCCGCTGACACGACGATCGGTGATTAAGCCGTTAGCCGTTAACTCTCCG 278  
468 AGTCCGCTGACACGACGATCGGTGATTAAGCCGTTAGCCGTTAGCCGTTAGCCG 409  
279 AAGACGACGATTTCCGCTGACCGCTGAGCGGACCGGACGTCGCGGTGAACCA 338  
408 AAGACGACGATTTCCGCTGACCGCTGAGCGGACCGGACGTCGCGGTGAACCA 349  
339 AAGACGACGATTTCCGCTGACCGCTGAGCGGACCGGACGTCGCGGTGAACCA 388  
348 AAGACGACGATTTCCGCTGACCGCTGAGCGGACCGGACGTCGCGGTGAACCA 289  
399 GTTGAATTTCTCTGTTTCCAGACCTTAAGACACATACATGCTCTTAAACATG 458  
288 TCTTCT 229  
459 AATTCGAGAAACATACCTTTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 508  
228 AAGACCTTAAGAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 169  
509 AAGACCTTAAGAACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 568  
168 CACATTAAGCACTGTGTGTT-GACACTCAATACCAAAATCTTAAGAAATGGCC 110  
569 CACATTTTC 576  
109 CACAGTTC 102

RESULT 12  
LOCUS BH774554 549 bp DNA linear GSS 28-MAR-2002  
DEFINITION uzmb003f010f02k0 uzmb unfiltered library Zea mays genomic clone  
ACCESSION BH774554  
VERSION BH774554.1 GI:19776612  
KEYWORDS GSS.  
SOURCE Zea mays.  
ORGANISM Zea mays

REFERENCE  
AUTHORS Budiman, M.A., Freese, R.G., Bedell, J.A., Nunberg, A.N. and Lakey, N.D.  
TITLE GeneThresher methylation filtered genomic sequences from maize  
JOURNAL Unpublished (2002)  
COMMENT Contact: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: uzmb003f010 row: f column: 02  
Seq primer: SK reverse  
Class: shotgun

High quality sequence stop: 549.  
Location/Qualifiers

## FEATURES

source

1..549  
/organism="Zea mays"  
/cultivar="W017"  
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/clone="uzmb003f010f02"  
/clone\_1ib="uzmb unfiltered library"  
/note="Organ: Leaf; Vector: pBSK(-); Site 1: HindIII; DNA  
prepared from purified nuclei was randomly sheared,  
end-repaired, size fractionated to enrich for the 0.5 to  
5 kb fraction, ligated into HindIII-digested pBSK(-)  
vector and electroporated into E. coli cells."

BASE COUNT 120 a 142 c 127 g 160 t  
ORIGIN

Query Match 11.2%; Score 288.4; DB 17; Length 549;  
Best Local Similarity 81.9%; Pred. No. 2.7e-59;  
Matches 367; Conservative 1; Mismatches 77; Indels 3; Gaps 3;

593 TGCCACACCGGACGATCCGCTGACCTCTGTTTAACTTGTGCGGCACT 652  
80 TGCTGTACCGGACGATCTGTGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 139  
653 GTTTCGACCTATAGCGTTTTCGACGACCGTTGGCGGACGACGACGACGACGACG 712  
140 GTTTCGACCTATAGCGTTTTCGACGACCGTTGGCGGACGACGACGACGACGACG 199  
713 GCTGACCGGACGATCCGATTAATATGCGGACGCGCTCTGAAATTTCCGAGTGG 772  
200 GCTGACCGGACGATCCGATTAATATGCGGACGCGCTCTGAAATTTCCGAGTGG 259  
773 TGTGTAAGGGGCGGCTGCGCGTGGACGACGACGACGACGACGACGACGACGAC 832  
260 TGTGTAAGGGGCGGCTGCGCGTGGACGACGACGACGACGACGACGACGACGAC 319  
833 ACTCAAGTCT 891  
320 ACTCA-TGTCTGCTCAATTTGATTGAGCCCTTAATTAATTTCTTCTGTTTGT 378  
892 GTTGAACCTTAAGCACTGAGATAATACATCTAGCAACAGTAAGTCAATGTTGT 951  
379 GTTGAACCTTAAGCACTGAGATAATACATCTAGCAACAGTAAGTCAATGTTGT 438  
952 TGTGTTGATCGCACTAATAATCTATTATAGAAAGTGTAAACCTATTTCCTTT 1011  
439 TGTGTTGATCGCACTAATAATCTATTATAGAAAGTGTAAACCTATTTCCTTT 497  
1012 CAGCACTCTATATATAGTGTGAGACC 1039  
498 CAATCT 525

RESULT 13  
LOCUS BH836722 620 bp DNA linear GSS 28-MAY-2002  
DEFINITION LMCR05003G04f Zea mays L. Zea mays genomic clone LMCR05003G04f.



DNA sequence.  
 BH836722  
 VERSION BH836722.1 GI:21234600  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 620)  
 Kim, S.W., Yu, Y., Lee, M.C., Main, D. and Wing, R.A.  
 Methyl-filtration genomic sequence from maize  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total High Quality bases = 501  
 Seq primer: TAAATACGACTCATTATAGCG  
 Class: shotgun  
 High quality sequence start: 7  
 High quality sequence stop: 614.  
 Location/Qualifiers  
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 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="LMCR050003G04F"  
 /clone\_1ib="Zea mays L."  
 /library\_type="Leaf"  
 /lab\_host="DH10B"  
 /note="Vector: pGEM-T easy; Site 1: Mcr BC; Methyl-filtration library; Nuclei DNA was completely digested with Mcr BC, size fractionated and transformed to E.Coli DH10B."  
 to E.Coli DH10B."

BASE COUNT 133 a 137 c 156 g 133 t 1 others  
 ORIGIN  
 Query Match 11.0%; Score 284.2; DB 17; Length 620;  
 Best Local Similarity 80.0%; Pred. No. 2.9e-58;  
 Matches 380; Conservative 0; Mismatches 73; Indels 22; Gaps 3;  
 QY 39 CGGATCTCTTCTTATTTGGGGAAGCCGCGTGGC-GCTTTGAGCGCGTTGGCGCAC 97  
 DB 121 CCGATTCTTCTTCTTACCGCGAAGCCGCGTGGGACGAGAGCGCGTTGGCGCAC 180  
 QY 98 CGGACCTGTCGGGTGACACCGGACAGTGAAGTGGCCCTTCCGACCGTTGGCTGGCC 157  
 DB 181 CGGACAT-----GTCGGGTGCCCCCTTTACCGCGTTGGCTGGCC 220  
 QY 158 ACCTGTTTCGCGGATTCGCGCGGAGACCGTGGCCGACGCGTGGGCTCACCCGA 217  
 DB 221 ACCTGTCGCGGAGATTCGCGCGGCGGACCGTGGCCGCGGCGGCGTGGCTCACCCGA 280  
 QY 218 CAGTCCGCGTGCACACGACAGATTCGCGGTGAATTATAGCCGTAGCCGTTAATCACTTCCC 277  
 DB 281 CAGTCCGCGTGCACACGACAGATTCGCGGTGAATTATAGCCGTAGCCGCGGATGAATCCC 340  
 QY 278 GAGAGAGCAAGTTGGCTGAGGCGGCGGCGGACCGGACACTGTCGCGTGAACACCG 337  
 DB 341 GAGAGAGCAAGTTGGCTGAGGCGGCGGCGGACCGGACACTGTCGCGTGAACACCG 400  
 QY 338 GACAGTCGCGTGCACCGAGTCAAGAGTGAATTGCTGAACAAAGTCATTTAGTTCCA 397  
 DB 401 GACAGTCGCGTGCACCGAGTCAAGAGTGAATTGCTGAACAAAGTCATTTAGTTCCA 459  
 QY 398 ACTGATTTTCTCTGTTTCCAGACTTAACACAAATATCTTGTCTTAAACAAATAT 457  
 DB 460 ATATGATCTTTCTCTGTTTCCATCACTTAGACAAATATAGTCTTAAACAAATATGAC 519

QY 458 TAATCTGAGAAACATACCTTATACCTTGTGACTTGTGTCACCAATTTACA 512  
 DB 520 TAACTGAGAAACATACCTTATACCTTGTGACTTGTGTCACCAATTTACA 574

RESULT 14  
 BH839302 813 bp DNA linear GSS 28-MAY-2002  
 LOCUS BH839302  
 DEFINITION LMCR150010G08F Zea mays L. Zea mays genomic clone LMCR150010G08F,  
 DNA sequence.  
 ACCESSION BH839302  
 VERSION BH839302.1 GI:21237317  
 KEYWORDS GSS.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 813)  
 Kim, S.W., Yu, Y., Lee, M.C., Main, D. and Wing, R.A.  
 Methyl-filtration genomic sequence from maize  
 JOURNAL Unpublished (2002)  
 COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total High Quality bases = 494  
 Seq primer: TAAATACGACTCATTATAGCG  
 Class: shotgun  
 High quality sequence stop: 667.  
 Location/Qualifiers  
 1..813  
 /organism="Zea mays"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="LMCR150010G08F"  
 /clone\_1ib="Zea mays L."  
 /library\_type="Leaf"  
 /lab\_host="DH10B"  
 /note="Vector: pGEM-T easy; Site 1: Mcr BC; Methyl-filtration library; Nuclei DNA was completely digested with Mcr BC, size fractionated and transformed to E.Coli DH10B."  
 to E.Coli DH10B."

FEATURES  
 source  
 BASE COUNT 172 a 240 c 185 g 216 t  
 ORIGIN  
 Query Match 11.0%; Score 283.2; DB 17; Length 813;  
 Best Local Similarity 78.8%; Pred. No. 5.1e-58;  
 Matches 462; Conservative 0; Mismatches 88; Indels 36; Gaps 9;  
 QY 37 TTGGATCTCTTCTTATTTGGGGAAGCCGCGTGGCGCTTTGAGCGCGTTGGCGCA 96  
 DB 87 TGGGATTTCTTCTTCTTATTTGGGGAAGCCGCGTGGGAGATTGAGAGCGCGTTGGCGCA 146  
 QY 97 CGGACCTGTCGGGTGACACCGGACAGTGAAGTGGCCCTTCCGACCGTTGGCTGGCC 137  
 DB 147 CCGACACTGTCGGGTGACACCGGACAGTGAAGTGGCCCTTCCGACCGTTGGCTGGCC 206  
 QY 138 TTCCGACCGTGGCTCGGCGGACAGTGTTCGCGGATTCGCGCGGACAGACCGTTGGCCGA 197  
 DB 207 TTCTAACCGTGGCTCGGCGGACAGTGTTCGCGGATTCGCGCGGACAGACCGTTGGCCGA 266  
 QY 198 CCGACCGTGGCTCGGCGGACAGTGTTCGCGGATTCGCGCGGACAGACCGTTGGCCGA 256  
 DB 267 CCGACCGTGGCTCGGCGGACAGTGTTCGCGGATTCGCGCGGACAGACCGTTGGCCGA 326  
 QY 257 GTAGCGCGTTAATCACTTCCGAGAGAGCAAGTGGCGTGGCGGACCGCGCGGCGG 316  
 DB 327 GTAGCGCGCGCA-GGAACCGAGAGAGCAAGTGGCGTGGCGGACCGCGCGGCGG 385

QY 317 AACTGTCGGTGAACCGGAGACGTCGGTGCACCCAGTCAAGCTGACTTTGGCTGA 376  
 Db 386 AACTGTCGGTGCACCGGAGACGTCGGTGCACCCAGTCAAGCTGACTTTGGCTGA 444  
 QY 377 ACAAGTCATCTTGAAGTTCCTCACTGATTTTCTGTTTCAGACACTAGACCAATACA 436  
 Db 445 GCTAGCGCAAGTCTTTTCCAAATGGCTTTCTGTTTCTAGACACTAGACCAATACA 504  
 QY 437 TTA-GTCTTAAACAAATGATTAATTCGAGAAACATACC-TTATATCTGTTGTATC 494  
 Db 505 TTAGTCTCCACTACATAGTACTAAGCTTAGAAACATACCTTTTACTCTTGAATTTGCAC 564  
 QY 495 TTTGTCCACCAT-----TTAACACTGGGCACTGTGTGACACTTAATACCA 544  
 Db 565 TTTTTCATCATTTTGGCATATGATTACACATGACACTGTGTGTG-CACTCATTTACCA 623  
 QY 545 AAATACCTTGAATGGCCAGGACATTTCCCTTCAACAGTCC 590  
 Db 624 AAAAATTG-AATGGCCAGAGGACATTTCCCTTTCATCTTCC 668

## RESULT 15

BH873660/c

618 bp DNA linear GSS 05-AUG-2002

hp46b1.1 b1 WGS-Zmaysf (JMI07 adapted methyl filtered) Zea mays

genomic clone hp46b1 5', DNA sequence.

BH873660

BH873660.1 GI:22109557

GSS.

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 618)

Rabinowitz,P.D., O'Shaughnessy,A.L., Ballia,V., Dedhia,N.,

Karzenburger,F., King,L., Miller,B., Miller,S., Nascimiento,L.,

Zuavevren,T., McCombie,W.R. and Martienssen,R.A.

Genomic shotgun sequences from Zea mays (methyl-filtered)

Unpublished (2002)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8874

Email: mcombie@cshl.org

Plate: hp46 row: b column: 11

Seq primer: -21M13UnivFwd

Class: shotgun

High quality sequence stop: 618.

Location/Qualifiers

1. 618

/organism="Zea mays"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone="hp46b1"

/clone\_lib="WGS-Zmaysf (JMI07 adapted methyl filtered)"

/lab\_host="JMI07 or DHSa"

/note="Organ: immature ears; Site\_1: Xba I; Site\_2: Xba I;

The vector was digested with XbaI and one nucleotide was

added by fill in in the recessive 3' end. The genomic DNA

was nebulized, end repaired, adaptor ligated and size

fractionated using sephadex. The resulting fragments were

between 0.8 and 3 kb and were cloned into the vector

(.x/y reads in M13mp19, .b/g reads in pUC19). The same

ligation was transformed in either JMI07 or DHSa."

BASE COUNT

ORIGIN

165 a 113 c 168 g 172 t

Query Match

Best Local Similarity

Matches 376; Conservative

10.9%; Score 282.2; DB 17; Length 618;

85.6%; Pred. No. 8.8e-58;

0; Mismatches 48; Indels 15; Gaps 5;

QY 157 CACGTTTTCGGGAGATCGCGGAGACCGTGGCCGACCGACCGTGGCTCACCG 216  
 Db 618 CATGTGTCTCCGCGAGATCGCGGAGACCGTGGCCGACCGTGGCTCACCG 559  
 QY 217 ACAATCCGGTGCACACGACGATCGCGTGAATTAAGCGGTATTCATCTTC 276  
 Db 558 ACAGTCGATGCAACCGGATGTTGGTGAATTAAGCGGTATTCATCTTC 499  
 QY 277 CGAGAGCAGCAAGTTCGCTGAGCGAGCGTGGCGACCGGACCTGTCCGCTGACAC 336  
 Db 498 CGAGGCTGCAAGTTCGCTGAGCGAGCGTGGCGACCGGACCTGTCCGCTGACAC 439  
 QY 337 GGAAGTCGGTGCACCGGAGTCAAGCT-GACTTGGCTGAACAAAGTCACTTATGTC 395  
 Db 438 GGAAGTCGGTGCACCGGAGTCAAGCT-GACTTGGCTGAACAAAGTCACTTATGTC 381  
 QY 396 CAATGATTTTCTGTTTCCAGCACTTAACACACATTAATCTTAAACAAATGT 455  
 Db 380 CAATGATTTTCTGTTTCCAGCACTTAACACACATTAATCTTAAACAAATGT 321  
 QY 456 ATTAATCTGAGAAACATACCTTTACTGTTGTACTTGTCCACCA----- 505  
 Db 320 ACTAAGTCTG-GAAACATACCTTTTAAATGATTTGCACTTGTCCACCACTTGCATAG 262  
 QY 506 TTTAACACTTGGGCACTTGTGTGAGCACTTAATACCAAAATCTTAAGAAATGCCCCA 565  
 Db 261 ATCAACACAAAAGGACTTGGCTTGG-CACTCAATACCAAAATCTTAAGAAATGCCCCA 203  
 QY 566 GGGCACATTTCCCTTTCAA 584  
 Db 202 GGGCACATTTCCCTTTCAA 184

Search completed: February 3, 2003, 16:08:28  
 Job time : 2388 secs